

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/591,045
Source: IFWP
Date Processed by STIC: 9/8/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 09/08/2006

PATENT APPLICATION: US/10/591,045

TIME: 14:47:52

Input Set : A:\22388WO.ST25.txt

Output Set: N:\CRF4\09082006\J591045.raw

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3 <110> APPLICANT: F. Hoffmann-La Roche AG
5 <120> TITLE OF INVENTION: Method for the recombinant expression of an N-terminal
fragment
6       of hepatocyte growth factor
8 <130> FILE REFERENCE: 22388 WO
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,045
C--> 10 <141> CURRENT FILING DATE: 2006-08-29
10 <150> PRIOR APPLICATION NUMBER: EP 04004951.2
11 <151> PRIOR FILING DATE: 2004-03-03
13 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1389
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1389)
26 <223> OTHER INFORMATION: DNA sequence encoding the alpha-chain of hepatocyte growth
factor
27       (HGF)
29 <400> SEQUENCE: 1
30  caa agg aaa aga aga aat aca att cat gaa ttc aaa aaa tca gca aag      48
31  Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
32  1             5             10             15
34  act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa aaa      96
35  Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
36             20             25             30
38  gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa gga      144
39  Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
40             35             40             45
42  ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa caa      192
43  Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
44             50             55             60
46  tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa gaa      240
47  Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
48  65             70             75             80
50  ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga aac      288
51  Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
52             85             90             95
54  tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc act      336
55  Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
56             100            105            110
58  aag agt ggc atc aaa tgt cag ccc tgg agt tcc atg ata cca cac gaa      384

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59 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu

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60	115	120	125	
62	cac agc ttt ttg cct tcg agc tat cgg ggt aaa gac cta cag gaa aac	432		
63	His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn			
64	130	135	140	
66	tac tgt cga aat cct cga ggg gaa gaa ggg gga ccc tgg tgt ttc aca	480		
67	Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr			
68	145	150	155	160
70	agc aat cca gag gta cgc tac gaa gtc tgt gac att cct cag tgt tca	528		
71	Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser			
72	165	170	175	
74	gaa gtt gaa tgc atg acc tgc aat ggg gag agt tat cga ggt ctc atg	576		
75	Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met			
76	180	185	190	
78	gat cat aca gaa tca ggc aag att tgt cag cgc tgg gat cat cag aca	624		
79	Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr			
80	195	200	205	
82	cca cac cgg cac aaa ttc ttg cct gaa aga tat ccc gac aag ggc ttt	672		
83	Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe			
84	210	215	220	
86	gat gat aat tat tgc cgc aat ccc gat ggc cag ccg agg cca tgg tgc	720		
87	Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys			
88	225	230	235	240
90	tat act ctt gac cct cac acc cgc tgg gag tac tgt gca att aaa aca	768		
91	Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr			
92	245	250	255	
94	tgc gct gac aat act atg aat gac act gat gtt cct ttg gaa aca act	816		
95	Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr			
96	260	265	270	
98	gaa tgc atc caa ggt caa gga gaa ggc tac agg ggc act gtc aat acc	864		
99	Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr			
100	275	280	285	
102	att tgg aat gga att cca tgt cag cgt tgg gat tct cag tat cct cac	912		
103	Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His			
104	290	295	300	
106	gag cat gac atg act cct gaa aat ttc aag tgc aag gac cta cga gaa	960		
107	Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu			
108	305	310	315	320
110	aat tac tgc cga aat cca gat ggg tct gaa tca ccc tgg tgt ttt acc	1008		
111	Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr			
112	325	330	335	
114	act gat cca aac atc cga gtt ggc tac tgc tcc caa att cca aac tgt	1056		
115	Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys			
116	340	345	350	
118	gat atg tca cat gga caa gat tgt tat cgt ggg aat ggc aaa aat tat	1104		
119	Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr			
120	355	360	365	
122	atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca atg tgg	1152		
123	Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp			
124	370	375	380	

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126 gac aag aac atg gaa gac tta cat cgt cat atc ttc tgg gaa cca gat      1200
127 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
128 385                      390                      395                      400
130 gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat gat gct      1248
131 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala
132                      405                      410                      415
134 cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg gat tat      1296
135 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
136                      420                      425                      430
138 tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca ata gtc aat      1344
139 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn
140                      435                      440                      445
142 tta gac cat ccc gta ata tct tgt gcc aaa acg aaa caa ttg cga      1389
143 Leu Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg
144 450                      455                      460
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 463
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 2
154 Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
155 1                      5                      10                      15
158 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
159 20                      25                      30
162 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
163 35                      40                      45
166 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
167 50                      55                      60
170 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
171 65                      70                      75                      80
174 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
175 85                      90                      95
178 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
179 100                     105                     110
182 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
183 115                     120                     125
186 His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn
187 130                     135                     140
190 Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr
191 145                     150                     155                     160
194 Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser
195 165                     170                     175
198 Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
199 180                     185                     190
202 Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
203 195                     200                     205
206 Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
207 210                     215                     220
210 Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys

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211 225          230          235          240
214 Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
215          245          250          255
218 Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
219          260          265          270
222 Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr
223          275          280          285
226 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
227          290          295          300
230 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
231 305          310          315          320
234 Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
235          325          330          335
238 Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
239          340          345          350
242 Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
243          355          360          365
246 Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
247          370          375          380
250 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
251 385          390          395          400
254 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala
255          405          410          415
258 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
259          420          425          430
262 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn
263          435          440          445
266 Leu Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg
267          450          455          460
270 <210> SEQ ID NO: 3
271 <211> LENGTH: 1350
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial
275 <220> FEATURE:
276 <223> OTHER INFORMATION: dna coding for NK4
279 <220> FEATURE:
280 <221> NAME/KEY: CDS
281 <222> LOCATION: (1)..(1350)
283 <400> SEQUENCE: 3
284 atg tct cgt aaa cgt cgt aat act att cat gaa ttc aaa aaa tca gca      48
285 Met Ser Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala
286 1          5          10          15
288 aag act acc cta atc aaa ata gat cca gca ctg aag ata aaa acc aaa      96
289 Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys
290          20          25          30
292 aaa gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa      144
293 Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys
294          35          40          45
296 gga ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa      192

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297	Gly	Leu	Pro	Phe	Thr	Cys	Lys	Ala	Phe	Val	Phe	Asp	Lys	Ala	Arg	Lys	
298		50					55					60					
300	caa	tgc	ctc	tgg	ttc	ccc	ttc	aat	agc	atg	tca	agt	gga	gtg	aaa	aaa	240
301	Gln	Cys	Leu	Trp	Phe	Pro	Phe	Asn	Ser	Met	Ser	Ser	Gly	Val	Lys	Lys	
302	65					70					75					80	
304	gaa	ttt	ggc	cat	gaa	ttt	gac	ctc	tat	gaa	aac	aaa	gac	tac	att	aga	288
305	Glu	Phe	Gly	His	Glu	Phe	Asp	Leu	Tyr	Glu	Asn	Lys	Asp	Tyr	Ile	Arg	
306				85						90					95		
308	aac	tgc	atc	att	ggg	aaa	gga	cgc	agc	tac	aag	gga	aca	gta	tct	atc	336
309	Asn	Cys	Ile	Ile	Gly	Lys	Gly	Arg	Ser	Tyr	Lys	Gly	Thr	Val	Ser	Ile	
310				100						105					110		
312	act	aag	agt	ggc	atc	aaa	tgt	cag	ccc	tgg	agt	tcc	atg	ata	cca	cac	384
313	Thr	Lys	Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	Ser	Ser	Met	Ile	Pro	His	
314			115					120						125			
316	gaa	cac	agc	ttt	ttg	cct	tcg	agc	tat	cgg	ggg	aaa	gac	cta	cag	gaa	432
317	Glu	His	Ser	Phe	Leu	Pro	Ser	Ser	Tyr	Arg	Gly	Lys	Asp	Leu	Gln	Glu	
318		130					135					140					
320	aac	tac	tgt	cga	aat	cct	cga	ggg	gaa	gaa	ggg	gga	ccc	tgg	tgt	ttc	480
321	Asn	Tyr	Cys	Arg	Asn	Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	Phe	
322	145					150					155					160	
324	aca	agc	aat	cca	gag	gta	cgc	tac	gaa	gtc	tgt	gac	att	cct	cag	tgt	528
325	Thr	Ser	Asn	Pro	Glu	Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	Cys	
326				165						170					175		
328	tca	gaa	gtt	gaa	tgc	atg	acc	tgc	aat	ggg	gag	agt	tat	cga	ggg	ctc	576
329	Ser	Glu	Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	
330				180					185						190		
332	atg	gat	cat	aca	gaa	tca	ggc	aag	att	tgt	cag	cgc	tgg	gat	cat	cag	624
333	Met	Asp	His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	
334			195					200						205			
336	aca	cca	cac	cgg	cac	aaa	ttc	ttg	cct	gaa	aga	tat	ccc	gac	aag	ggc	672
337	Thr	Pro	His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	
338		210					215						220				
340	ttt	gat	gat	aat	tat	tgc	cgc	aat	ccc	gat	ggc	cag	ccg	agg	cca	tgg	720
341	Phe	Asp	Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	
342	225					230					235					240	
344	tgc	tat	act	ctt	gac	cct	cac	acc	cgc	tgg	gag	tac	tgt	gca	att	aaa	768
345	Cys	Tyr	Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	
346				245						250					255		
348	aca	tgc	gct	gac	aat	act	atg	aat	gac	act	gat	gtt	cct	ttg	gaa	aca	816
349	Thr	Cys	Ala	Asp	Asn	Thr	Met	Asn	Asp	Thr	Asp	Val	Pro	Leu	Glu	Thr	
350				260					265						270		
352	act	gaa	tgc	atc	caa	ggg	caa	gga	ggc	tac	agg	ggc	act	gtc	aat		864
353	Thr	Glu	Cys	Ile	Gln	Gly	Gln	Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Val	Asn	
354			275					280						285			
356	acc	att	tgg	aat	gga	att	cca	tgt	cag	cgt	tgg	gat	tct	cag	tat	cct	912
357	Thr	Ile	Trp	Asn	Gly	Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	Pro	
358		290					295					300					
360	cac	gag	cat	gac	atg	act	cct	gaa	aat	ttc	aag	tgc	aag	gac	cta	cga	960
361	His	Glu	His	Asp	Met	Thr	Pro	Glu	Asn	Phe	Lys	Cys	Lys	Asp	Leu	Arg	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date